

Outline of Microarray Chip Technology approach

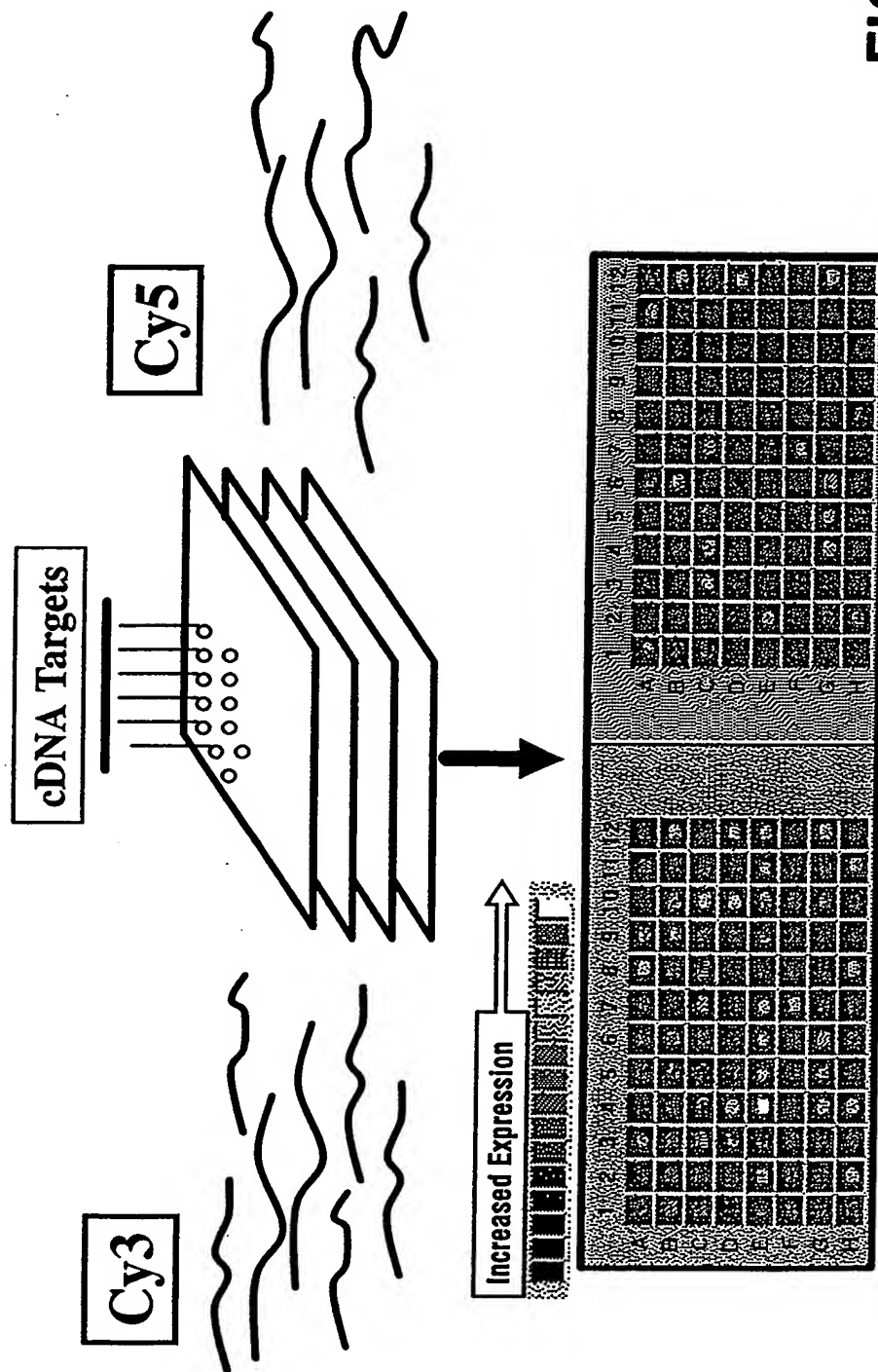


FIG. 1

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General protocol for *in-vitro* whole gene CD8 T cell priming

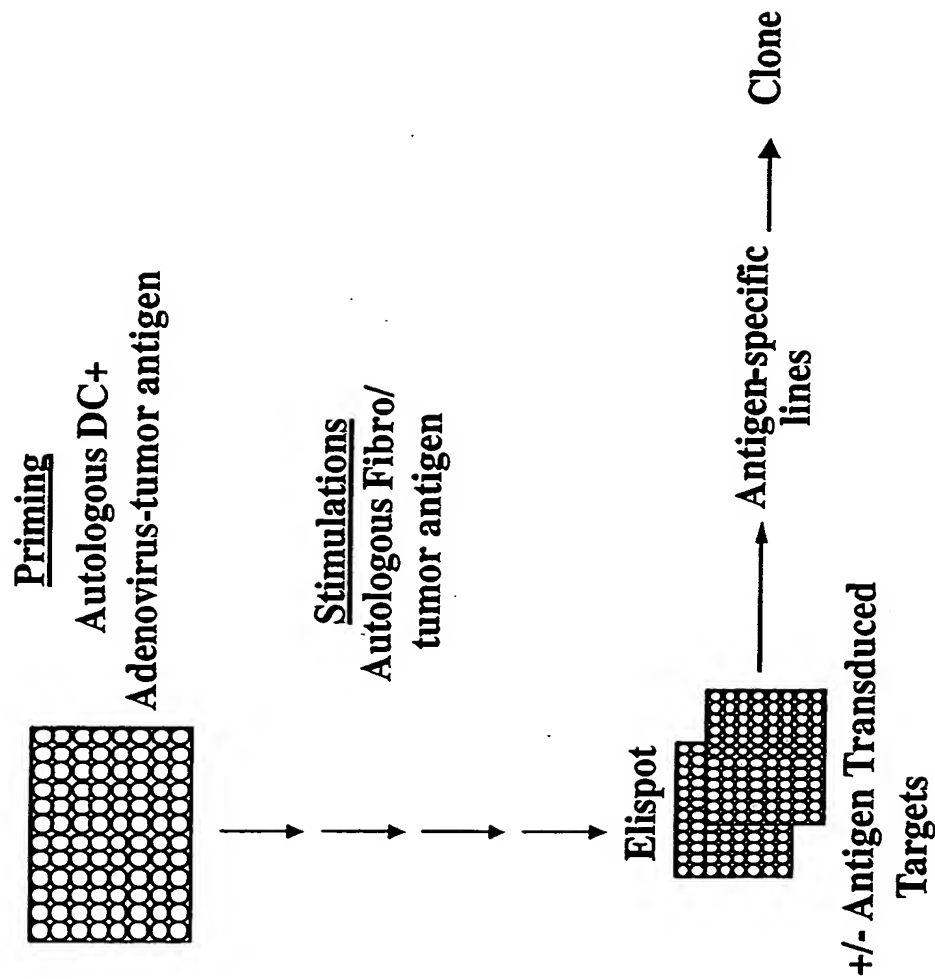


FIG. 2

General protocol for *in-vitro* whole gene CD4 T cell priming

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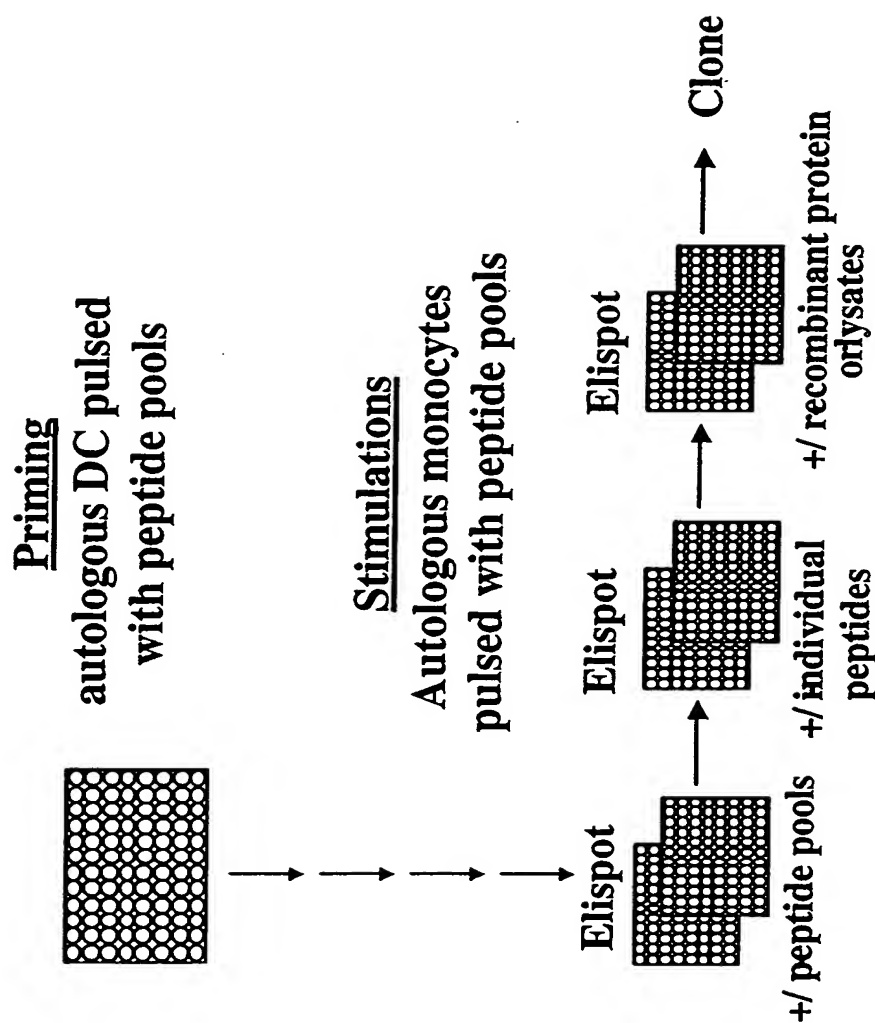


FIG. 3

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LEUKEMIA/LYMPHOMA CHIP #3: PROBES USED IN ANALYSIS

Cy3 Probe		Cy5 Probe	
Tissue	RNA#	RNA#	Tissue
Lymphoma, T cell	952	SPACT74	Kidney N
Lymphoma, B cell	955	SPACT81	Liver N
Lymphoma, B cell	953	SPACT78	Lung N
Lymphoma	916	SPACT42	Brain N
Lymphoma, Hodgkins	950	138598B	Skin N
Lymphoma, Hodgkins	950	SPACT49	Bone Marrow N
Lymphoma, B cell	CL151	888	PBMC resting
Lymphoma, T cell	904B	SPACT55	Stomach N
Lymphoma, Hodgkins see RNA 959	CL153	SPACT70	Thymus N
Lymphoma, B cell	CL152	SPACT75	Skeletal Muscle N
Lymphoma, B cell see RNA 958	CL155	SPACT73	Heart N
Lymphoma, B cell	944	243502B	Esophagus N
Lymphoma, B cell	958	1006	Colon N
Lymphoma, B cell	954	SPACT65	Small Intestine N
Lymphoma	960	779B	Trachea N
Lymphoma, T cell	957	S9327328	Bladder N
Lymphoma, B cell	914B		
Lymphoma, B cell	913		
Lymphoma, B cell	944B		
Lymphoma, B cell/failed	903		

GREEN: Tumor probes where gene expression would be desired.**RED:** Normal essential tissue probes where gene expression is to be avoided.**BLACK:** Normal tissue probes where gene expression is acceptable.**FIG. 4**

Hematology Therapeutic Ab Candidates

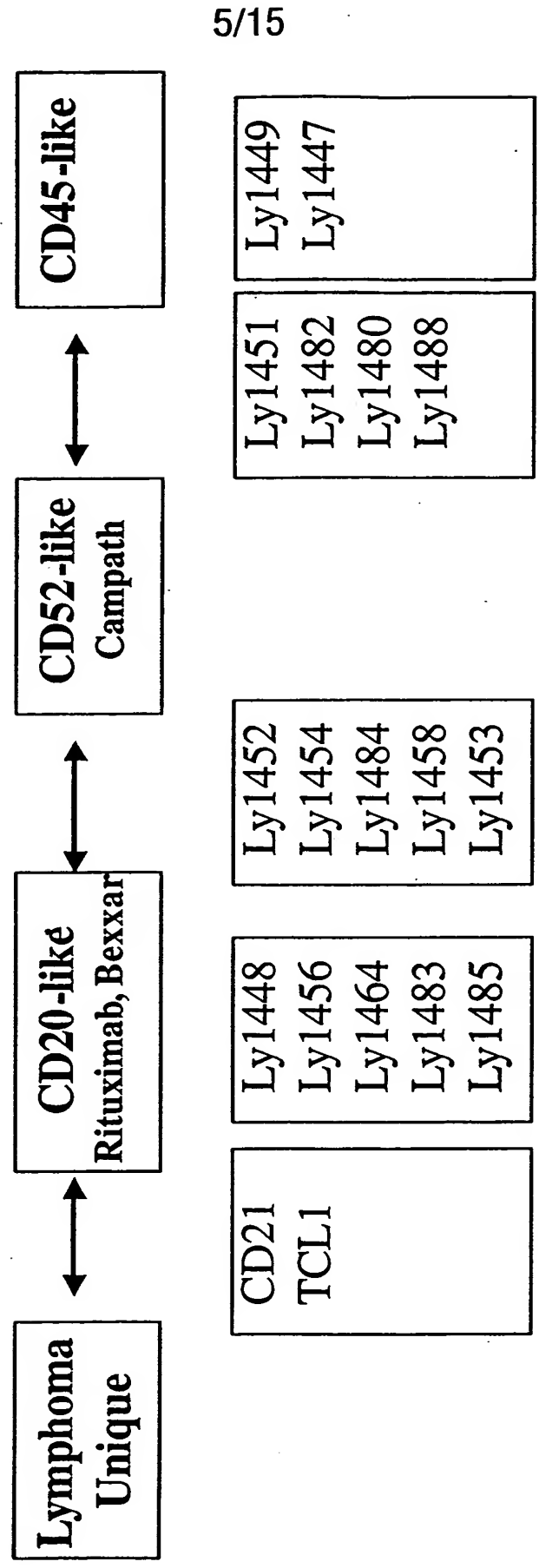


FIG. 5

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a. TMpred Report for Ly1484 Long

RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPQPSAEAAAAPSLANISCF
 TQKLVEKLYSGMFSADPRHLLLFILLEHIMVVIE TASSORDIVLSTLYSSL
 NKVILYCLSKPQOOSLSECLGLLSILGLFLOEHWDVVFAT YNSNISFLLCLM
 HCLLLLNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSDV
 QHNIQKTVQTLWQQLVAQRQQTLEDAFKIDLSVKPGEREVKIEEVTPLWE
 ETMLKAWQHYLASEKKSLASRSNVAHHSKVTLWSGSLSSAMKLMPGRQAK
 DPECKTEDFVSCIENYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQ
 EQLFGELGLWSQGEETKPCSPWELDWREGPARMRKRIKRLSPLEALSSGR
 HKESQDKNDHISQTNAENQDELTLREAEGEPDEVGVDCTQLTFFPALHES
 LHSEDFLELCRERQVILQELLDKKVTQKFSLVIVQGHVSEGVLLFGHQ
 HFYICENFTLSPTECDVYCHRHCLSNISDPFIFNLCSKDRSTEDHYSCQCHS
 YADMRELROARFLLQDIALEIFFHNGYSKFLV FYNNDRSKAFKSFCSFQP
 SLKGKATSEDTLNLRRYPGSDRIMLQKWQKRDISNFEYLMYLNNTAAGRTC
 NDYMQYPVFPWVLADYTSETLNLANPKIFRDLSKPMGAQTKERKLKFIQR
 FKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPPTQAFCALQ GCSFD
 VADRMFHSVKSTWESASRENMSDVRELTPPEFFYLPEFLHNCNEVEFGCMQ
 DGTVLCDVQLPPWADEDPRKFISLHRKALESDFVSANLHHWIDLIFCYKQ
 QCPAAVDAVNIFHPYFYCDRMDLSSITDPLIKSTILGFVSNFCQVPKQLF
 TKPHPARTAACKPLPKDVDSTPVSLLPCHPQPFYSLQSLRPSQVIVKDMY
 LFSLGESESPKCAITHTVSTETKTLAVERNKVLLPPLWNRTFSWGFDDFSC
 CLCSYGSDDKVLMTFENLAAWGRCLCAVCPSPTTIVTSETSTVVCVWELSM
 TKCRPRCLRLRQALYCHTQAVTCLAASVTFSLVSGESQDCTCTLLNDLHL
 THVTRLPAHREGTSAITISDVSETIVSCAGHLSLWNVNGOPLASTTAW
 GPEGAITCCCLMECPAWDTSQIITITESQDGMVRVWKTEEDVKMSVPCRPA
 EEPLAQPPSPRGHKWEKNLALSRELDVSTALTECKPSKTS PAVTALAVSRN
 HFKLLVCDERERTFCWSADG (SEQ ID NO: 120)

Black = INTRACELLULAR, Red = TRANSMEMBRANE,
 Blue = EXTRACELLULAR

Ly1484 Long has 1269 amino acids and 5

Transmembrane Domains

Transmembrane Domain 1: 63 - 84	Score: 1.36675
Transmembrane Domain 2: 118 - 139	Score: 1.38695
Transmembrane Domain 3: 480 - 501	Score: 1.36185
Transmembrane Domain 4: 562 - 583	Score: 1.31785
Transmembrane Domain 5: 725 - 746	Score: 1.3521

FIG. 6

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b. TMpred Report for Ly1484 (short)

MLQKWQKRDISNFEYLMYLNNTAAGRTCNDYMQYPVFPWVLADYTSETLNL
 ANPKIFRDLSKPMGAQTKERKLKFIQRFKEVEKTEGDMTVQCHYYTHYSS
 AIIVASYLVRMPFFTQAFCA~~Q~~CGSFDVADRMFHSVKSTWESASRENMSD
 VRELTP~~EFFYLPEFL~~ENCNEVEFGCMODGTVLEDVOLPPWADGDP~~RKFIS~~
 LHRKALESDFVSANLHHWIDLTFCYKQOCPAAVDAVNIFHPYFYCDRMDL
 SSITDPLIKSTILCFVSNFCQVPKOLFTEKPHPARTAACKPLPKGDVSTPV
 SLPCHPOPFYSLQSLRPSQVTVKDMYLFSLGSESPKCAIGHIVST~~EKTI~~
 LAVERNKVLLPPLWNRTFSWGFDDFSCCLGSYCS~~DKVLM~~TFENLA~~AWERC~~
 LCAVCPSP~~TTIVIS~~GETSTVVCVWELSMTEKCRPRCLRLROALYCHTQAVTC
 LAASVTFSLLVSGSQDCTCTLDLDHILTHVTRLPAHREGTS~~AITISDVSC~~
 TIVSCACAHLSLWNVNGOPLASTTAWCPEGATTCCLMECPAWDTSQIT
 ITCSQDGMVRVWKTEDVKMSVPCRPAGEEPLAOPPSPRCHKWEKNLALSR
 ELDVSTAL~~TC~~KPSKTS~~PAV~~TALAVSRNH~~EKLLV~~GEDERGRIFCWSADG

(SEQ ID NO: 121)

Black = INTRACELLULAR, Red = TRANSMEMBRANE,
 Blue = EXTRACELLULAR

Ly1484 has 646 amino acids and 1 Transmembrane
 Domains

Transmembrane Domain 1: 102 - 123 Score: 1.3521

FIG. 6 (cont.)

ANALYSIS RESULTS OF THE PROGRAM TSITES.

[illegible]

These are the results of the analysis of the file--> LY1484~1.TXT
Beginning with residue: 1 and ending with residue: 1270
AMPHI Window size: 11

A-AMPHI mid points of blocks.
R-Residues matching the Rothbard/Taylor motif.
D-Residues matching the IAd motif.
d-Residues matching the IEd motif.

[illegible]**FIG. 7**

FIG. 7 (cont.)

```

455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LHSEDFLELCRERQVILQELLDKEKVTQKFSLVIVQGHLVSEGVLIFGHQHFYICENFTLSPTGVDVYCTRHCLSN
...AAAAA...RRRR..RRRR..RRRR..RRRR..RRRR..RRRR..RRRR..RRRR..RRRR..RRRR..AAAA
530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
ISDPFIFNLCKDRSTDHYSCQCHSYADMRELROARFLLQDIALEIFFHNHNGYSKFLVFYNNDRSKAFFKSFCSFQP
A.AAAAAA.....AAAAAA.....RRRRRRRRRRRR.....RRRR.....
605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
SLKGKATSETLNLRYPGSDRIMLKWQKRDISNFEYLMYLNTAAGRTCNDYMQVPFPWLADYTSETLNLAN
.....AAAAA.....AAA.....AAAAAA....RRRRRRRR..RRRRRRRR..DDDDDD
680 685 690 695 700 705 710 715 720 725 730 735 740 745 750
PKIFRDLSKPMGAQTAKERKLKFIORFKEVEKTEGDMTVQCHYYTHYSSAIIVASLYVRMPPTQAFCALQGSFD
AAAAAAAAAAAA.....AAAAAA.....RRRR.RRRRR..RRRR.RRRRR..RRRR.RRRRR..RRRR.RRRRR..

```

FIG. 7 (cont.)

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```

.....DDDDDDDDDD.....
.....ddd.....
755 760 765 770 775 780 785 790 795 800 805 810 815 820 825
VADRMFHSVKSTWESASRENMSDVRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGDVQLPPWADGDPKRFISLH
AAAAAAA.AA.AAAA.AAAAAA.....AAA.....RRRRR.....RRRR..
RRRRRR.....RRRR.....RRRR.....RRRR.....RRRR.....
.....
.....
830 835 840 845 850 855 860 865 870 875 880 885 890 895 900
RKALESDFVSANLHHWIDLIFGYKQQGPAAVDAVNIFHPYFYGDRMDLSSITDPLIKSTILGFVSNFGQVPKQLF
.....AAAAAAA.....AAAAAAA.....AAAAA.....AAAAAAA.....
.RRRR.RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....
.....DDDDDD.....
.....
905 910 915 920 925 930 935 940 945 950 955 960 965 970 975
TKPHPARTAAGKPLPGKDVSTPVSPLPGHPQPFYSLQSLRPSQVTVKDMYLFSLGSESPKGAIGHIVSTEKTILA
.....AAAAAAA.....AAAAA.....RRRR.....RRRRRR.....
.....RRRR.....RRRR.....RRRR.....RRRR.....
.....DDDDDD.....DDDDDD.....
.....

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FIG. 7 (cont.)

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980 985 990 995 1000 1000 1010 1015 1020 1025 1030 1030 1040 1045 1050
VERNKVLLPPLWNRFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAVCPSTTIVTSGTSTVVCWELSM
.....AAAAA.....
RRRR.....
.....DDDDDDDDDD.....DDD
.....
1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125
TKGRPRGLRLRQALYGHTQAVTCLAAASVTFSLVSGSDCTCILWDLDHLTHVTRLPAHREGISAITISDVSGTI
.....AAAAA.....AAA...AAA
RRRRRR.....RRR
DDD...DDDDDD.....DDDDDD.....DDDDDD
.dddddd.....
1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200
VSCAGAHLSLWNVNGQPLASITTAWGPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG
A.....AAA.....AAAAAA
RR.....RRRR.....RRRRRR
D.....DDDDDD.....DDDDDD.....DDDDDD
.....
1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275
EEPLAQPPSPRGHKWEKNLALSRELDVSIALTGKPSKTSPAVTALAVSRNHTKLLVGDERGRIFCWSADG
.....RRRR
.....DDDDDDDD.....DDDDDD
.....

```

FIG. 7 (cont.)

ANALYSIS RESULTS OF THE PROGRAM TSITES.

FIG. 8

These are the results of the analysis of the file--> LY1484~2.TXT
Beginning with residue: 1 and ending with residue: 647
AMPHI Window size: 11

A-AMPHI mid points of blocks.
R-Residues matching the Rothbard/Taylor motif.
D-Residues matching the IAd motif.
d-Residues matching the IEd motif.

(SEQ ID NO: 121)

5	10	15	20	25	30	35	40	45	50	55	60	65	70	75
MLQKWQKRDISNFEYLMYLNTAAGRTCNDYMQVPVFPWVLADYTS	ETLNLANPKIFRDL	SKPMGAQTKERKLKFI												
AAA	AAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAA
RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRR
ddd	ddd	ddd	ddd	ddd	ddd	ddd	ddd	ddd	ddd	ddd	ddd	ddd	ddd	ddd

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80	85	90	95	100	105	110	115	120	125	130	135	140	145	150
QRFKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPPTQAF	CALQGSF	VDVADRMFHSVKSTWESASRENMSD												
AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AA
RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRR
DDD	DDD	DDD	DDD	DDD	DDD	DDD	DDD	DDD	DDD	DDD	DDD	DDD	DDD	DDD

155	160	165	170	175	180	185	190	195	200	205	210	215	220	225
VRELTPEFFYLPFLTNCNGVEFGCMQDGTVLGDVQLPPWADG	DPKFFISLHRKALESDFVSANLHHWIDLIFGY													
AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA
RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRRR	RRR
RRR	RRR	RRR	RRR	RRR	RRR	RRR	RRR	RRR	RRR	RRR	RRR	RRR	RRR	RRR

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230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
KQGPAAVDVNIHFHYPFYGDRLSSITDPLIKSTILGFVSNFGQVPKQLFTKPHPARTAAGKPLPGKDVSTPV
...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA
RRRR...RRRR...RRRR...RRRR...RRRR...RRRR...RRRR...RRRR...RRRR...RRRR
...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD
...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD

305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
SLPGHPQPFYSLQSLRPSQVTVKDMYLFSLGSESPKGAIGHIVSTEKILAVERNKVLLPPLWNRTFSWGFDDE
AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA
RRRRRRRR...RRRRRRRR...RRRRRRRR...RRRRRRRR...RRRRRRRR...RRRRRRRR
D...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD
...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD

380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
SCCLGSYGSDKVLMTFENLAAWGRCCLCAVCPSTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAVTC
...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA
RRRRR...RRRRR...RRRRR...RRRRR...RRRRR...RRRRR...RRRRR...RRRRR
...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD
...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD...DDDDD

455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LAASVTFSLVSGSQDCTCILWDLDHLTHVTRLPAHREGISAITISDVSGTIVSCAGAHLSLWNVNGQPLASIT
...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA...AAAAA
RRRRRRR...RRRRRRR...RRRRRRR...RRRRRRR...RRRRRRR...RRRRRRR...RRRRRRR...RRRRRRR
DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD
...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD...DDDDDDDD

```

FIG. 8 (cont.)

```

530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
AWGPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAGEEPLAQPPSPRGHKWEKNLALSR
.....AAAAAAA
RRRR.....
D.....DDDDDD
.....

605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
ELDVSIALTGKPSKTSPAVTALAVSRNHTKLLVGDERGRIFCWSADG
.....RRRR.....
DDDDDDDD.....ddddd
.....

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FIG. 8 (cont.)

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